Revista Ciência Agronômica, v. 48, n. 5 (Especial), p. 889-896, 2017
Centro de Ciências Agrárias - Universidade Federal do Ceará, Fortaleza, CE
www.ccarevista.ufc.br

Artigo Científico
ISSN 1806-6690

Selection of cowpea populations tolerant to water deficit by selection index[1]

Seleção de populações de feijão-caupi tolerantes ao déficit hídrico por índice de seleção

Erina Vitório Rodrigues[2], Kaesel Jackson Damasceno-Silva[3]*, Maurisrael de Moura Rocha[3], Edson Alves Bastos[3] and Paulo Eduardo Teodoro[4]

ABSTRACT - The objective of this work was to use different selection criteria to identify cowpea genotypes tolerant to water deficit to be used in recurrent selection programs aiming to reduce the cowpea crop cycle and improve its productive components. Six cowpea genotypes were crossed in a complete diallel scheme. The experiment was conducted in an incomplete block experimental design in a triple lattice arrangement, with the 30 F_2 populations of cowpea. The genetic variability of 10 traits was verified, and the following selection criteria were used: direct and indirect selection, classical index, index based on desired gains, and index based on sum of ranks. The number of days to flowering (NDF), number of days to maturity (NDMD), pod weight (PW), grain weight per pod (GWP) and 100-grain weight (100GW) were classified as primary traits, and the others as secondary. The direct selection based on the pod weight was the most efficient criterion to reduce the crop cycle and improve productive components of the cowpea genotypes subjected to water deficit conditions. The genotypes Pingo-de-Ouro-1-2 × MNC99-510F-16-1, CNCx698-128G × MNC99-510F-16-1, MNC99-510F-16-1 × Pingo-de-Ouro-1-2, Pingo-de-Ouro-1-2 × BRS Paraguaçu, Santo-Inácio × Pingo-de-Ouro-1-2, BRS Xiquexique × Pingo-de-Ouro-1-2 and Pingo-de-Ouro-1-2 × Santo-Inácio were the most suitable to be used in interpopulation recurrent selection programs aiming to reduce the crop cycle and improve productive components of cowpea grown under water deficit conditions.

Key words: Direct and indirect selection. Interpopulation recurrent selection. *Vigna unguiculata* L. Walp.

RESUMO - O objetivo desse trabalho foi utilizar diferentes critérios de seleção para identificar genótipos de feijão-caupi tolerantes ao déficit hídrico, a serem utilizados em programas de seleção recorrente, visando redução do ciclo e incremento nos componentes produtivos. Seis genótipos de feijão-caupi foram cruzados no esquema dialélico completo. Foi conduzido um ensaio em delineamento experimental de blocos incompletos em arranjo do tipo látice triplo para avaliar as 30 populações F_2 de feijão-caupi. Após verificar variabilidade genética para 10 caracteres, empregaram-se os seguintes critérios de seleção: seleção direta e indireta, índice clássico, índice baseado nos ganhos desejados e índice baseado em soma de *ranks*. Os caracteres número de dias para o início de floração (NDIF), número de dias para a maturidade (NDMD), peso da vagem (PV), peso de grãos por vagem (PGV), peso de 100 grãos (PCG) foram considerados como primários, e os demais como secundários. A seleção direta com base no caráter peso de vagem é o critério mais eficiente para reduzir o ciclo e incrementar os componentes produtivos em genótipos de feijão-caupi submetidos ao déficit hídrico. Os genótipos Pingo de Ouro-1-2 x MNC99-510F-16-1, CNCx 698-128G x MNC99-510F-16-1, MNC99-510F-16-1 x Pingo de Ouro-1-2, Pingo de Ouro-1-2 x BRS Paraguaçu, Santo Inácio x Pingo de Ouro-1-2, BRS Xiquexique x Pingo de Ouro-1-2 e Pingo de Ouro-1-2 x Santo Inácio são os mais indicados para serem utilizados em programas de seleção recorrente interpopulacional, visando redução do ciclo e aumento nos componentes produtivos do feijão-caupi, quando submetido ao déficit hídrico.

Palavras-chave: Seleção direta e indireta. Seleção recorrente interpopulacional. *Vigna unguiculata* (L.) Walp.

DOI: 10.5935/1806-6690.20170105
* Autor para correspondência
Recebido para publicação em 14/08/2016; aprovado em 28/06/2017
[1]Parte da Tese de Mestrado do primeiro autor apresentada ao Programa de Pós-Graduação em Genética e Melhoramento, Departamento de Fitotecnia, Universidade Federal do Piauí, Teresina-PI, Brasil
[2]Programa de Pós-Graduação em Genética e Melhoramento, Departamento de Fitotecnia, Universidade Federal do Piauí, Teresina-PI, Brasil, erina.rodrigues@colaborador.embrapa.br
[3]Embrapa Meio-Norte, Caixa Postal 01, Teresina-PI, Brasil, 64.006-220, kaesel.damasceno@embrapa.br, maurisrael.rocha@embrapa.br, edson.bastos@embrapa.br
[4]Departamento de Biologia Geral, Laboratório de Biometria, Universidade Federal de Viçosa/UFV, Viçosa-MG, Brasil, eduteodoro@hotmail.com

INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp] is one of the most important and strategic food sources in tropical and subtropical regions of the world (AGBICODO *et al.*, 2009). Brazil is the third largest world producer of this crop, which is cultivated in the North and Northeast regions of the country and is the basic food of low-income populations (OLIVEIRA *et al.*, 2013). However, according to Almeida *et al.* (2014), there are frequent supply deficits in these regions due to the cowpea low national average yield (300 kg ha^{-1}).

The low yield of cowpea in Brazil is due to several factors, such as the use of unimproved genotypes, the low fertility of the soils and irregular rainfall distribution (NASCIMENTO *et al.*, 2011). Water deficit is common in these regions of Brazil and is one of the factors that reduce the cowpea yield (MENDES *et al.*, 2007). Agbicodo *et al.* (2009) point out that the cowpea 'drought scape' by shortening its cycle is one of the main mechanism used by this species to avoid water deficit. Therefore, identifying genotypes with early cycles is one of the most promising strategies to minimize the water deficit in this crop.

Different agronomic traits have been used to investigate the tolerance of cowpea genotypes to water deficit (BASTOS *et al.*, 2011; NASCIMENTO *et al.*, 2011). The simultaneous selection of traits increases the chance of success in breeding programs. Selection indexes allow the generation of a genotypic aggregate as an additional trait resulting from the linear combination of traits chosen by the breeder as desirable to perform the simultaneous selection; thus allowing the identification of superior genotypes, regardless of correlations between the traits (CRUZ; REGAZZI; CARNEIRO, 2012).

In this context, the objective of this work was to use different selection criteria to identify cowpea genotypes tolerant to water deficit to be used in intrapopulation recurrent selection programs aiming to reduce the cowpea crop cycle and improve its productive components.

MATERIAL AND METHODS

The experiment was conducted in the experimental area of the Embrapa Meio-Norte, in Teresina PI, Brazil (05° 05'S, 42° 48'W and 74.4 m), from July 26 to October 11, 2011. Teresina has annual average relative humidity of 77.02%, annual average rainfall of 1,388.9 mm, and annual average air temperature of 26.97 ºC (22.08 ºC to 33.52 ºC) (INMET, 2011). The climate of the region is Aw—tropical with wet and dry seasons—according to the Köppen classification. The soil of the experimental area was classified as eutrophic Yellow Argisol (Ultisol), according to the SiBCS, with sandy loam surface texture.

Six genotypes of cowpea—three cultivars (BRS Paraguaçu, BRS Xiquexique and Santo-Inácio) and three lines (Pingo-de-Ouro-1-2, CNCx698-128G and MNC99-510F-16-1)—were selected based on previous studies on tolerance to water deficit (BASTOS *et al.*, 2011; NASCIMENTO *et al.*, 2011) and used as parents (Table 1). These genotypes were crossed in a complete diallel scheme, according to Method 1 of the model proposed by Griffing (1956). The seeds of the 30 F_1 hybrids were seeded to obtain the F_2 generation.

A water deficit test was conducted to evaluate the 30 F_2 populations of cowpea and their parents. An incomplete block experimental design in a triple lattice arrangement was used. The experimental plot consisted of six 2-m rows spaced 1.0 m apart with 0.50 m between plants. Irrigation was performed with a fixed conventional system with sprinklers in lateral lines arranged in a spacing of 12 m x 12 m, with pressure of 250 kPa, nozzle diameter of 3.6 mm x 2.6 mm, and flow rate of 1.19 $m^3 h^{-1}$.

Soil moisture was monitored using a capacitance probe (DIVINER 2000®) with 12 access tubes that were installed to a depth of 0.70 m and distributed in both tests, with readings at each 0.10 m depth of the soil. The soil water retention curve of the experimental area—0.0 to 0.4 m layer—was determined using the model of Genuchten (1980). The area had field capacity (FC) of 21.2 cm^3 cm^{-3} and permanent wilt point (PWP) of 9.05 cm^3 cm^{-3}. The water deficit test (WDT) was conducted with suspension of irrigation from the pre-flowering at 35 days after sowing (DAS) to the reproductive stage at 49 DAS.

Data were collected from 15 random plants from each plot. The mean values of the following traits were evaluated in each plot: number of days to flowering (NDF)—number of days from sowing to the beginning of flowering stage; number of days to maturation (NDM)—number of days between flowering and the physiological maturity stage of the pod; number of days to field maturity (NDMD)—number of days from sowing to the beginning of the drying process (appearance of the first pod with color change); number of peduncles per plant (NPeP); number of pods per plant (NPoP); number of pods per peduncle (NPPe); pod weight per plant (PWP)—using 3 pods per plant (g); pod weight (PW)—using 3 pods per plant (g); pod length (PL)— using 3 pods per plant (cm); number of grains per pod (NGP)— using 3 pods per plant; grain weight per pod (GWP)— using 3 pods per plant (g); 100-grain weight (100GW) (g); grain yield (GY) (g); and grain index (GI)—grain to pod weight ratio (%).

Table 1 - Parents and hybrids of cowpea genotypes evaluated under water deficit conditions

Identification	Genotypes		
1	BRS Paraguaçu		
2	Pingo-de-Ouro-1-2		
3	BRS Xiquexique		
4	CNCx698-128G		
5	Santo-Inácio		
6	MNC99-510F-16-1		
7	BRS Paraguaçu	×	Pingo-de-Ouro-1-2
8	BRS Paraguaçu	×	BRS Xiquexique
9	BRS Paraguaçu	×	CNCx698-128G
10	BRS Paraguaçu	×	Santo-Inácio
11	BRS Paraguaçu	×	MNC99-510F-16-1
12	Pingo-de-Ouro-1-2	×	BRS Paraguaçu
13	Pingo-de-Ouro-1-2	×	BRS Xiquexique
14	Pingo-de-Ouro-1-2	×	CNCx698-128G
15	Pingo-de-Ouro-1-2	×	Santo-Inácio
16	Pingo-de-Ouro-1-2	×	MNC99-510F-16-1
17	BRS Xiquexique	×	BRS Paraguaçu
18	BRS Xiquexique	×	Pingo-de-Ouro-1-2
19	BRS Xiquexique	×	CNCx698-128G
20	BRS Xiquexique	×	Santo-Inácio
21	BRS Xiquexique	×	MNC99-510F-16-1
22	CNC×698-128G	×	BRS Paraguaçu
23	CNC×698-128G	×	Pingo-de-Ouro-1-2
24	CNC×698-128G	×	BRS Xiquexique
25	CNC×698-128G	×	Santo-Inácio
26	CNC×698-128G	×	MNC99-510F-16-1
27	Santo-Inácio	×	BRS Paraguaçu
28	Santo-Inácio	×	Pingo-de-Ouro-1-2
29	Santo-Inácio	×	BRS Xiquexique
30	Santo-Inácio	×	CNCx698-128G
31	Santo-Inácio	×	MNC99-510F-16-1
32	MNC99-510F-16-1	×	BRS Paraguaçu
33	MNC99-510F-16-1	×	Pingo-de-Ouro-1-2
34	MNC99-510F-16-1	×	BRS Xiquexique
35	MNC99-510F-16-1	×	CNCx698-128G
36	MNC99-510F-16-1	×	Santo-Inácio

The data obtained for each trait were subjected to analysis of variance, according to the model: $Y_{ijk} = m + g_i + r_j + b_{k(j)} + e_{ijk}$, wherein Y_{ijk} is the observed value in the plot that received the treatment i in the block k within the replication j; m is the overall mean; g_i is the random effect of treatment i (i = 1, 2, ..., 36); r_j is the effect of the replication j (j = 1, 2 and 3); $b_{k(j)}$ is the effect of the block k (k = 1, 2, 3, ..., 6) within the replication j; and e_{ijk} is the experimental error of the observation Y_{ij} with ~ NID $(0,\sigma^2)$. The following genetic parameters were estimated

for each trait according to the procedures described by Cruz, Regazzi and Carneiro (2012): heritability in the broad sense (h^2), genetic standard deviation (SDg), genetic coefficient of variation (CVg) and relative coefficient of variation (CVr).

First, a multicollinearity diagnosis was performed in the matrices of phenotypic (P) and genotypic variance and covariance, in which the number of conditions showed a weak multicollinearity (NC<100). The economic weights and desired gains were established from the experimental data, as recommended by Cruz, Regazzi and Carneiro (2012), to predict the genetic gain in the main traits. The adopted desired gain was equivalent to the genetic standard deviation (SDg), and the adopted economic weights were the genetic coefficient of variation (CVg) estimates. The selection of the best genotypes and estimations of genetic progress were performed with the following methods: direct and indirect selection, classical index (HAZEL, 1943; SMITH, 1936), index based on the desired gains (PESEK; BAKER, 1969) and index based on the sum of ranks (MULAMBA; MOCK, 1978).

The direct and indirect selection is used expecting gains in a single trait, which is focused in the selection, and traits of secondary importance may have favorable or unfavorable responses. The expected gain from the direct selection in the i^{th} trait was estimated by: $GS_i = DS_i h_i^2$, being $DS_i = (\bar{X}_{si} - \bar{X}_{oi})$, wherein X_{si} is the mean of the selected genotypes for the trait *i*; X_{0i} is the original mean of the diallel; DS_i is the selection differential practiced in the diallel; and h^2_1 is the heritability of the trait *i*. The indirect gain in trait *j* by the selection of the trait *i* was given by: $GS_{j(i)} = DS_{j(i)} h^2_i$, wherein $DS_{j(i)}$ is the indirect selection differential obtained with the mean of the trait of the genotypes, whose superiority was shown based on other trait on which direct selection is practiced.

The classical index proposed by Smith (1936) and Hazel (1943) consists of a linear combination of several economically important traits whose weighting coefficients are estimated in order to maximize the correlation between the genotypic aggregate and the index. The genotypic aggregate is established by another linear combination, involving the genetic values that are weighted by their respective economic weights (CRUZ; REGAZZI; CARNEIRO, 2012). The selection index of Smith (1936) and Hazel (1943) is given by: $I_{SH} = \sum_{i=1}^{n} b_i X_i = b'X$, wherein *n* is the number of traits evaluated; *b'* is the vector of dimension $1 \times n$ of the weighting coefficients of the selection index to be estimated; *x* is the matrix of dimension $n \times p$ (genotypes) of phenotypic values of the trait. The genotypic aggregate is estimated by $H = \sum_{i=1}^{n} a_i g_i = a'g$ wherein a' is the vector of dimension $1 \times n$ of economic weights previously established; and *g* is the matrix of dimension $n \times p$ of unknown genetic values of the *n* trait. Thus, the vector $b = P^{-1} Ga$, wherein P^{-1} is the inverse of the matrix of dimension $n \times n$ of phenotypic variance and covariance between the traits; and *G* is the matrix of dimension $n \times n$ of genetic variance and covariance between the traits.

The Pesek and Baker (1969) index is based on the desired gains for the traits, defined by $\Delta g = \frac{Gbi}{\sigma_1}$. Substituting Δg, the vector of the estimated gains, by Δg_d, the vector of the desired gains, and eliminating the scalar i/σ_1, which does not affect the proportionality of the coefficients *b's*, *b* is estimated by the expression $DS_i = (\bar{X}_{si} - \bar{X}_i$, whose coefficients give the maximization of the gains in each trait based on the specification of the desired gains. Subsequently, the genotypic aggregates were estimated by $I_{PB} = \sum_{i=1}^{n} b_i x_i = b'x$, wherein *n* is the number of traits evaluated; *b'* is the vector of dimension $1 \times n$ of the weighting coefficients of the selection index to be estimated; *x* is the matrix of dimension $n \times p$ (genotypes) of the phenotypic values of the trait.

The index based on sum of ranks (MULAMBA; MOCK, 1978) consists of classifying the genotypes regarding each of the traits in order of improvement. Then, the orders of each genotype are summed, resulting in the selection index $I_{MM} = \sum_{j=1}^{n} r_j$, wherein r_j is the rank of the genotype *i* regarding the j^{th} trait; *n* is the number of traits in the index.

Eight genotypes were selected for each case, corresponding to an intensity of approximately 22%. Statistical analysis were performed with the Genes (CRUZ, 2013) and SAS (SAS INSTITUTE, 2002) programs.

RESULTS AND DISCUSSION

The evaluated traits of the genotypes presented significant differences (p<0.05), except NDM, NPeP, PWP and GY (Table 2). The existence of genetic variability in a population is a determining factor for any breeding program, thus, the cowpea genotypes evaluated are promising for recurrent selection for tolerance to water deficit. Recent studies also identified genetic variability among cowpea genotypes (BASTOS *et al.*, 2011; CORREA *et al.*, 2012; HAMIDOU; ZOMBRE; BRACONNIER, 2007; NASCIMENTO *et al.*, 2011; RODRIGUES *et al.*, 2016; SANTOS *et al.*, 2014; TEODORO *et al.*, 2016; TORRES *et al.*, 2015).

According to Cruz, Regazzi and Carneiro (2012), the experimental precision is high when the experimental coefficient of variation (CVe) estimates of the traits with continuous distribution are lower than 20%, as found in this study. The lattice design presented high efficiency—except for NGP and GI—according to the criteria of Ramalho, Ferreira and Oliveira (2005),

who define as adequate the use of this experimental design in situations where the efficiency is higher than 100.

The genetic coefficient of variation (CVg) quantifies the genetic variability available for selection (CRUZ; REGAZZI; CARNEIRO, 2012). The ratio between CVg and CVe is the relative coefficient of variation (CVr). The CVg obtained resulted in a CVr higher than 1 for NDF, NDMD, NPPe, PW, PL, GWP, 100GW and GI. This is a favorable situation for the selection of superior genotypes in the populations. The heritability (h^2) estimates for these traits—except NDMD—can be considered high (>70%) because they are polygenic traits, governed by several genes of small effect on the phenotype.

Variability among the traits included in the index is essential to employ selection indices in plant breeding (CRUZ; REGAZZI; CARNEIRO, 2012). Therefore, NDM, NPeP, PWP and GY were not included in the indices used in this work; NDF, NDMD, PW, GWP and 100GW were considered as primary and the others as secondary parameters for the prediction of genetic gain. This choice was made considering that an ideal cowpea genotype has a reduced cycle, which makes it possible to be cultivated in times with lower water availability, and have high grain weight, since this trait affects its commercialization.

The gains predicted by the direct selection were superior to the indirect gains for all the traits, and close in situations in which the traits are highly correlated, for example, for PW, GWP and 100GW (Table 3). Falconer (1987) reports that indirect selection can promote greater gains than direct selection, when the auxiliary trait presents greater heritability than the main one, and when the genetic correlation between them is positive and of high magnitude. The highest individual gains were observed for 100GW (14.30), NPPe (13.17) NPoP (9.83), and PW (8.38%).

Among the traits used for direct and indirect selection, PW was the most promising for use in recurrent selection programs with these genotypes; it promoted reduction in the NDF and NDMD and increased in the PW, GWP and 100GW. The genotypes selected according to this criterion were Pingo-de-Ouro-1-2 × MNC99-510F-16-1, CNCx698-128G × MNC99-510F-16-1, MNC99-510F-16-1 × Pingo-de-Ouro-1-2, Pingo-de-Ouro-1-2, BRS Paraguaçu, Santo-Inácio × Pingo-de-Ouro-1-2, BRS Xiquexique × Pingo-de-Ouro-1-2, Pingo-de-Ouro-1-2 × Santo-Inácio. Thus, these genotypes can be used in intrapopulational recurrent selection programs aiming to improve resistance to water deficit. These results are desirable in breeding programs of cowpea because the reduction of the crop cycle is one of the main physiological mechanisms of tolerance to water deficit

Table 2 - Analysis of variance and genetic parameters for number of days to flowering (NDF), number of days to field maturity (NDMD), number of days to maturation (NDM), number of peduncles per plant (NPeP), number of pods per plant (NPoP), number of pods per peduncle (NPPe), pod weight per plant (PWP), pod weight (PW), pod length (PL), number of grains per pod (NGP), grain weight per pod (GWP), grain yield (GY), 100-grain weight (100GW), and grain index (GI) of 36 cowpea genotypes grown under water deficit conditions

SV	DF	NDF	NDMD	NDM	NPeP	NPoP	NPPe	PWP	PW	PL	NGP	GWP	GY	100GW	GI
							Mean Squares								
Replication	2	4.75	34.48	19.75	67.66	211.02	0.03	2003.37	0.08	2.61	1.72	0.02	290518.14	0.76	0.42
Block/Replication	15	4.79	1.57	2.95	33.33	92.51	0.04	966.48	0.30	1.62	0.86	0.15	139085.41	6.12	6.83
Treatment (adjusted)	35	3.28*	1.68*	1.71^{ns}	12.35^{ns}	48.33*	0.05*	349.68^{ns}	0.40*	2.82*	2.84*	0.20*	50892.41^{ns}	11.87*	19.03*
Error	55	0.76	0.41	1.11	9.78	21.54	0.01	275.60	0.15	0.50	0.87	0.05	35940.47	0.86	5.10
CVe (%)		2.25	1.12	5.76	16.41	16.66	6.21	19.24	10.32	3.43	6.11	7.70	19.51	4.66	2.84
Efficiency		120.55	125.23	100.76	121.65	128.03	101.58	128.09	100.37	107.27	99.19	102.62	132.24	100.68	89.47
							Genetic parameters								
h^2 (%)		74.05	45.57	74.32	9.53	46.02	87.05	44.18	83.25	81.35	69.42	73.96	4.71	93.58	78.06
SDg		1.02	0.56	0.22	0.69	3.00	0.14	4.54	0.82	0.15	1.09	0.24	30.01	2.09	2.32
CVg (%)		2.62	3.07	1.19	3.62	10.76	9.62	5.26	11.93	4.49	5.30	7.84	3.09	10.51	2.92
CVr		1.16	2.74	0.21	0.22	0.65	1.55	0.27	1.16	1.31	0.87	1.02	0.16	2.26	1.03

^{ns} = not significant by the F test, * = significant at 5% probability by the F test, and ** = significant at 1% probability by the F test. SV = sources of variation; DF = degrees of freedom; CVe = experimental coefficient of variation; h^2 = heritability; SDg = genetic standard deviation; CVg = genetic coefficient of variation; CVr = relative coefficient of variation

Table 3 - Estimates of the means ($\dot{X}_0$), heritability (h^2) and selection gains (%) obtained by direct and indirect selection in the traits number of days to flowering (NDF), number of days to maturity (NDMD), number of pods per plant (NPoP), number of pods per peduncle (NPPe), pod weight (PW), pod length (PL), number grains per pod (NGP), grain weight per pod (GWP), 100-grain weight (100GW) and grain index (GI) of 36 cowpea genotypes grown under water deficit conditions

Trait	$\dot{X}_0$	h^2 (%)	NDF	NDMD	NPoP	NPPe	PW	PL	NGP	GWP	100GW	GI
NDF	38.77	74.05	-2.69	2.05	5.86	2.20	-4.43	-1.12	0.24	-5.29	7.49	-1.22
NDMD	57.18	45.57	1.32	-2.22	0.31	1.77	-2.18	-0.73	1.28	-0.72	-2.54	1.04
NPoP	27.84	46.02	-1.81	0.87	9.83	8.03	-2.88	0.31	1.71	-4.28	-7.97	-0.40
NPPe	1.46	87.05	-1.73	0.24	8.15	13.17	-3.45	0.64	1.15	-3.48	-6.13	0.76
PW	3.84	63.25	0.76	0.22	-2.37	-4.26	8.38	-1.07	-1.50	6.01	10.70	-0.56
PL	20.50	81.34	0.28	-0.24	-0.12	2.47	0.24	4.65	2.63	2.71	-0.58	1.59
NGP	15.31	69.42	0.90	-0.72	0.86	4.75	2.03	3.17	5.55	2.62	-4.48	1.72
GWP	3.02	73.96	0.60	0.03	-3.39	-4.16	6.41	0.87	0.34	7.71	9.93	1.25
100GW	19.91	93.58	0.65	-0.02	-4.19	-5.05	6.44	-0.74	-3.28	6.88	14.30	0.36
GI	79.54	78.06	0.36	-1.20	1.06	7.14	-1.41	2.86	4.68	1.97	-3.89	2.96

(AGBICODO *et al.*, 2009). In addition, the indirect response in the other traits suggests the possibility of selecting genotypes with high grain yield.

The estimates of gains predicted by the Smith (1936) and Hazel (1943), Pesek and Baker (1969), and Mulamba and Mock (1978) indexes are described in Table 4. In general, the estimates using the Smith (1936) and Hazel (1943) and Mulamba and Mock (1978) indexes are similar in magnitude and direction. This generated the coincident selection of the genotypes 2, 13, 15, 16, 18, 28, 33 and 34. The Pesek and Baker (1969) index showed gains with similar magnitudes to the other indices used for PW, GWP and 100GW, however, it showed different magnitudes and direction from the predicted gains for the other traits.

According to Cruz, Regazzi and Carneiro (2012) the use of selection indexes is advantageous compared to the direct selection, since it allows more distributed gains in all evaluated traits without providing significant loss in the main traits. However, in the present work, none

Table 4 - Estimations of selection gains (%) obtained by the Smith (1936) and Hazel (1943), Pesek and Baker (1969) and Mulamba and Mock (1978) indexes in the traits number of days to flowering (NDF), number of days to maturity (NDMD), number of pod per plant (NPoP), number of pods per peduncle (NPPe), pod weight (PW), pod length (PL), number of grains per pod (NGP), grain weight per pod (GWP), 100-grain weight (100GW) and grain index (GI) of 36 cowpea genotypes grown under water deficit conditions

Traits	X_o	h^2 (%)	Smith and Hazel	Pesek and Baker	Mulamba and Mock
NDF	38.77	74.05	1.55	-0.15	0.68
NDMD	57.18	45.57	-0.90	1.19	-0.22
NPoP	27.84	46.02	-10.31	0.58	-2.56
NPPe	1.46	87.05	-3.57	0.73	-3.14
PW	3.84	63.25	8.50	6.11	6.39
PL	20.50	81.34	1.00	2.06	0.39
NGP	15.31	69.42	-2.96	0.50	-1.95
GWP	3.02	73.96	9.55	8.46	7.15
100GW	19.91	93.58	13.31	12.70	12.48
GI	79.54	78.06	1.80	-0.58	0.73
Selected genotypes			2, 16, 15, 13, 28, 33, 34 and 18	6, 11, 27, 1, 9, 25, 30 and 7	18, 2, 33, 16, 28, 34, 32 and 13

of the selection indices used was efficient in selecting genotypes that simultaneously provide reduction in cycle related traits and increase in the traits PW, GWP and 100GW. Similar results were observed by Santos and Araújo (2001) using different selection indices in cowpea genotypes; they found that the direct selection in productive traits provided greater gains on the others, when compared to the Smith (1936) and Hazel (1943), Pesek and Baker (1969) and Mulamba and Mock (1978) indexes.

CONCLUSIONS

1. Direct selection based on the pod weight trait is the most efficient criterion to reduce the cycle and increase the productive components in cowpea genotypes subjected to water deficit conditions;
2. The genotypes Pingo-de-Ouro-1-2 × MNC99-510F-16-1, CNCx698-128G × MNC99-510F-16-1, MNC99-510F-16-1 × Pingo-de-Ouro-1-2, Pingo-de-Ouro-1-2, BRS Paraguaçu, Santo-Inácio × Pingo-de-Ouro-1-2, BRS Xiquexique × Pingo-de-Ouro-1-2, and Pingo-de-Ouro-1-2 × Santo-Inácio are the most suitable to be used in recurrent selection programs aiming to reduce the crop cycle and improve productive components of cowpea grown under water deficit conditions.

REFERENCES

AGBICODO, E. M. *et al*. Breeding drought tolerant cowpea: constraints, accomplishments, and future prospects. **Euphytica**, v. 167, p. 353-370, 2009.

ALMEIDA, W. S. *et al.* Correlation and path analysis in components of grain yield of cowpea genotypes. **Revista Ciência Agronômica**, v. 45, p. 726-736, 2014.

BASTOS, E. A. *et al*. Identification of cowpea genotypes for drought tolerance. **Revista Ciência Agronômica**, v. 42, n. 1, p. 100-107, 2011.

CORREA, A. M. *et al.* Estimativas de parâmetros genéticos e correlações entre caracteres fenológicos e morfoagronômicos em feijão-caupi. **Revista Ceres**, v. 59, p. 88-94, 2012.

CRUZ, C. D. Genes: a software package for analysis in experimental statistics and quantitative genetics. **Acta Scientiarum**, v. 35, n. 3, p. 271-276, 2013.

CRUZ, C. D.; REGAZZI, A. J.; CARNEIRO, P. C. S. **Modelos biométricos aplicados ao melhoramento genético**. 4. ed. Viçosa, MG: UFV, 2012. 480 p.

FALCONER, D. S. **Introdução à genética quantitativa**. Trad. de Martinho de Almeida e Silva e José Carlos Silva. Viçosa, MG: UFV: Imprensa Universitária, 1987. 279 p.

GENUCHTEN, M. T. A closed form equation for predicting hydraulic conductivity of unsaturated soils. **Soil Science Society of American Journal**, n. 44, p. 892-898, 1980.

GRIFFING, B. Concept of general and specific ability in relation to diallel crossing systems. **Australian Journal of Biological Sciences**, v. 9, p. 462-93, 1956.

HAMIDOU, F.; ZOMBRE, G.; BRACONNIER, S. Physiological and biochemical responses of cowpea genotypes to water stress under glasshouse and field conditions. **Journal of Agronomy and Crop Science**, v. 193, p. 229-237, 2007.

HAZEL, L. N. The genetic basis for constructing selection indexes. **Genetics**, v. 28, p. 476-490, 1943.

INSTITUTO NACIONAL DE METEOROLOGIA. Dados meteorológicos. 2011. Disponível em: <http://www.inmet.gov.br/>. Acesso em: 10 fev. 2012.

MENDES, R. M. S. *et al.* Relações fonte-dreno em feijãode-corda submetido à deficiência hídrica. **Revista Ciência Agronômica**, v. 38, n. 1, p. 95-103, 2007.

MULAMBA, N. N.; MOCK, J. J. Improvement of yield potential of the Eto Blanco maize (*Zea mays* L.) population by breeding for plant traits. **Egyptian Journal of Genetics and Cytology**, v. 7, p. 40-57, 1978.

NASCIMENTO, S. P. *et al.* Tolerância ao déficit hídrico em genótipos de feijão-caupi. **Revista Brasileira de Engenharia Agrícola e Ambiental**, v. 15, n. 8, p. 853-860, 2011.

OLIVEIRA, O. M. S. *et al.* Associações genotípicas entre componentes de produção e caracteres agronômicos em feijão-caupi. **Revista Ciência Agronômica**, v. 44, p. 851-857, 2013.

PESEK, J.; BAKER, R. J. Desired improvement in relation to selected indices. **Canadian Journal of Plant Science**, v. 49, p. 803-804, 1969.

RAMALHO, M. A. P.; FERREIRA, D. F.; OLIVEIRA, A. C. **Experimentação em genética e melhoramento de plantas**. 2. ed. Lavras: UFLA, 2005. 322 p.

RODRIGUES, E. V. *et al*. Diallelic analysis to obtain cowpea (*Vigna unguiculata* L. Walp.) populations tolerant to water déficit. **Genetics and Moleceular Research**, v. 15, n. 2, p. 1-8, 2016.

SANTOS, C. A. F.; ARAÚJO, F. P. Aplicação de índices para seleção de caracteres agronômicos de feijão-de-corda. **Revista Ciência Agronômica**, v. 32, n. 1/2, p. 78-84, 2001.

SANTOS, J. A. S. *et al.* Desempenho agronômico e divergência genética entre genótipos de feijão-caupi cultivados no ecótono Cerrado/Pantanal. **Bragantia**, v. 73, p. 377-382, 2014.

SAS INSTITUTE. SAS Software. Version 9.1. Cary, North Carolina: SAS Institute Inc., 2002.

SMITH, H. F. A discriminant function for plant selection. **Annual Eugenics**, v. 7, p. 240-250, 1936.

TEODORO, P. E. *et al*. Measurements of experimental precision for trials with cowpea (*Vigna unguiculata* L. Walp.) genotypes. **Genetics and Moleceular Research**, v. 15, n. 2, p. 1-8, 2016.

TORRES, F. E. *et al*. Número de repetições para avaliação de caracteres em genótipos de feijão-caupi. **Bragantia**, v. 74, n. 2, p.161-168, 2015.